

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/773,455A
Source: IFWO
Date Processed by STIC: 10/16/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/16/2006

PATENT APPLICATION: US/10/773,455A

TIME: 11:40:00

Input Set : A:\08919-111001.txt

Output Set: N:\CRF4\10162006\J773455A.raw

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4 <110> APPLICANT: Shyur, Lie-Fen
5      Wen, Tuan-Nan
6      Lee, Shu-Hua
7      Yang, Ning-Sun
9 <120> TITLE OF INVENTION: Truncated 1,3-1,4-Beta-D-Glucanase
12 <130> FILE REFERENCE: 08919-111001
14 <140> CURRENT APPLICATION NUMBER: US 10/773,455A
15 <141> CURRENT FILING DATE: 2004-02-06
17 <150> PRIOR APPLICATION NUMBER: US 09/654,652
18 <151> PRIOR FILING DATE: 2000-09-05
20 <160> NUMBER OF SEQ ID NOS: 22
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 349
26 <212> TYPE: PRT
27 <213> ORGANISM: Fibrobacter succinogenes
29 <400> SEQUENCE: 1
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31 1          5          10          15
32 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly
33          20          25          30
34 Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr Gly Lys Phe Glu Ala
35          35          40          45
36 Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe Leu
37          50          55          60
38 Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
39 65          70          75          80
40 Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile
41          85          90          95
42 Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala
43          100         105         110
44 Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr Tyr Gly Leu Glu Trp
45          115         120         125
46 Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg Lys
47          130         135         140
48 Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
49 145          150         155         160
50 Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp
51          165         170         175
52 Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr
53          180         185         190
54 Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser Asp Phe Thr Leu Asp
55          195         200         205

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56 Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys Gly
57      210                      215                      220
58 Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
59 225                      230                      235                      240
60 Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln
61                      245                      250                      255
62 Glu Ser Phe Asn Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln
63                      260                      265                      270
64 Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser
65                      275                      280                      285
66 Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser Ser
67      290                      295                      300
68 Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
69 305                      310                      315                      320
70 Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn
71                      325                      330                      335
72 Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
73      340                      345
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 27
78 <212> TYPE: PRT
79 <213> ORGANISM: Fibrobacter succinogenes
81 <400> SEQUENCE: 2
82 Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala
83 1      5      10      15
84 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala
85      20      25
88 <210> SEQ ID NO: 3
89 <211> LENGTH: 175
90 <212> TYPE: PRT
91 <213> ORGANISM: Fibrobacter succinogenes
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94 Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
95 1      5      10      15
96 Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val
97      20      25      30
98 Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg
99      35      40      45
100 Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser
101      50      55      60
102 Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser
103 65      70      75      80
104 Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
105      85      90      95
106 Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly
107      100      105      110
108 Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly
109      115      120      125
110 Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp

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111      130      135      140
112 Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn
113 145      150      155      160
114 Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly
115      165      170      175
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 64
120 <212> TYPE: PRT
121 <213> ORGANISM: Fibrobacter succinogenes
123 <400> SEQUENCE: 4
124 Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly
125 1      5      10      15
126 Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp
127      20      25      30
128 Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala
129      35      40      45
130 Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val Pro Arg Asp
131      50      55      60
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 78
136 <212> TYPE: PRT
137 <213> ORGANISM: Fibrobacter succinogenes
139 <400> SEQUENCE: 5
140 Gln Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser
141 1      5      10      15
142 Ser Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser
143      20      25      30
144 Ser Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala
145      35      40      45
146 Val Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val
147      50      55      60
148 Asn Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
149 65      70      75
152 <210> SEQ ID NO: 6
153 <211> LENGTH: 1050
154 <212> TYPE: DNA
155 <213> ORGANISM: Fibrobacter succinogenes
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (1)...(1047)
161 <400> SEQUENCE: 6
162 atg aac atc aag aaa act gca gtc aag agc gct ctc gcc gta gca gcc 48
163 Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala
164 1      5      10      15
166 gca gca gca gcc ctc acc acc aat gtt agc gca aag gat ttt agc ggt 96
167 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly
168      20      25      30
170 gcc gaa ctc tac acg tta gaa gaa gtt cag tac ggt aag ttt gaa gcc 144
171 Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr Gly Lys Phe Glu Ala

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172	35	40	45	
174	cgt atg aag atg gca gcc gca tcg gga aca gtc agt tcc atg ttc ctc	192		
175	Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe Leu			
176	50	55	60	
178	tac cag aat ggt tcc gaa atc gcc gat gga agg ccc tgg gta gaa gtg	240		
179	Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val			
180	65	70	75	80
182	gat att gaa gtt ctc ggc aag aat ccg ggc agt ttc cag tcc aac atc	288		
183	Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile			
184	85	90	95	
186	att acc ggt aag gcc ggc gca caa aag act agc gaa aag cac cat gct	336		
187	Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala			
188	100	105	110	
190	gtt agc ccc gcc gcc gat cag gct ttc cac acc tac ggt ctc gaa tgg	384		
191	Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr Tyr Gly Leu Glu Trp			
192	115	120	125	
194	act ccg aat tac gtc cgc tgg act gtt gac ggt cag gaa gtc cgc aag	432		
195	Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg Lys			
196	130	135	140	
198	acg gaa ggt ggc cag gtt tcc aac ttg aca ggt aca cag gga ctc cgt	480		
199	Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg			
200	145	150	155	160
202	ttt aac ctt tgg tcg tct gag agt gcg gct tgg gtt ggc cag ttc gat	528		
203	Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp			
204	165	170	175	
206	gaa tca aag ctt ccg ctt ttc cag ttc atc aac tgg gtc aag gtt tat	576		
207	Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr			
208	180	185	190	
210	aag tat acg ccg ggc cag ggc gaa ggc ggc agc gac ttt acg ctt gac	624		
211	Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser Asp Phe Thr Leu Asp			
212	195	200	205	
214	tgg acc gac aat ttt gac acg ttt gat ggc tcc cgc tgg ggc aag ggt	672		
215	Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys Gly			
216	210	215	220	
218	gac tgg aca ttt gac ggt aac cgt gtc gac ctc acc gac aag aac atc	720		
219	Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile			
220	225	230	235	240
222	tac tcc aga gat ggc atg ttg atc ctc gcc ctc acc cgc aaa ggt cag	768		
223	Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln			
224	245	250	255	
226	gaa agc ttc aac ggc cag gtt ccg aga gat gac gaa cct gct ccg caa	816		
227	Glu Ser Phe Asn Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln			
228	260	265	270	
230	tct tct agc agc gct ccg gca tct tct agc agt gtt ccg gca agc tcc	864		
231	Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser			
232	275	280	285	
234	tct agc gtc cct gcc tcc tcg agc agc gca ttt gtt ccg ccg agc tcc	912		
235	Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser Ser			
236	290	295	300	

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238 tcg agc gcc aca aac gca atc cac gga atg cgc aca act ccg gca gtt .960
239 Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
240 305 310 315 320
242 gca aag gaa cac cgc aat ctc gtg aac gcc aag ggt gcc aag gtg aac 1008
243 Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn
244 325 330 335
246 ccg aat ggc cac aag cgt tat cgc gtg aac ttt gaa cac taa 1050
247 Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
248 340 345
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 248
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Synthetic construct
259 <400> SEQUENCE: 7
260 Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu
261 1 5 10 15
262 Glu Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala
263 20 25 30
264 Ser Gly Thr Val Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile
265 35 40 45
266 Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys
267 50 55 60
268 Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
269 65 70 75 80
270 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln
271 85 90 95
272 Ala Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp
273 100 105 110
274 Thr Val Asp Gly Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser
275 115 120 125
276 Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu
277 130 135 140
278 Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
279 145 150 155 160
280 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly
281 165 170 175
282 Glu Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr
283 180 185 190
284 Phe Asp Gly Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn
285 195 200 205
286 Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu
287 210 215 220
288 Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
289 225 230 235 240
290 Pro Arg Asp Asp Glu Pro Ala Pro
291 245
294 <210> SEQ ID NO: 8

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VERIFICATION SUMMARY

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